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AmpC β-lactamase producing Escherichia coli associated with urinary tract infection from a tertiary health care centre in North East India

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Background: *Escherichia coli* are the major causes of urinary tract infection (UTI) and an emerging problem worldwide. These organisms harbouring AmpC beta-lactamase is a major cause of therapeutic failure leaving cephalosporins inactive along with co-existing mechanism of resistance. The aim of this study was to investigate the prevalence of *Escherichia coli* producing AmpC beta-lactamase in UTI and analyse their antibiotic susceptibility pattern from a tertiary care hospital in North Eastern part of India.

Methods & Materials: A total of 126 *Escherichia coli* were biochemically identified from a 293 consecutive non repetitive clini-cal isolates which were obtained from patient with UTI over a period of 12 months (February2013 to January 2014). Isolates were initially screened with cefoxitin (30 μg) and confirmed for production of AmpC beta-lactamases by M3DET. Phenotypically positive isolates were further confirmed by multiplex PCR targeting bla_{CIT}, bla_{ACC}, bla_{EBC}, bla_{DHA}, bla_{FOX}, bla_{MOX} families Antimicrobial susceptibility and MIC's were also determined as per CLSI guideline.

Results: Out of 126 *Escherichia coli* isolates 97(76.9%) were found to be cefoxitin resistant and among them 46 (47.4%) isolates were confirmed to be AmpC producers. Most of the AmpC positive isolates were found to be significantly multi-drug resistant and their minimum inhibition concentrations were above the break point. Out of 46 isolates 39 (84.7%) showed genotypically positive for $bla_{AmpC\,genes}$ (24CIT, 12DHA and 3EBC).

Conclusion: In the present study AmpC β-lactamase production is accompanied by multi drug resistance therefore, therapeutic options become limited resulting a need for new measures for the management of *Escherichia coli* causing urinary tract infections

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Antibiotic resistance among hospitalized patients in Mauritius in 2014

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Background: A retrospective survey of bacteria isolated from hospitalised patients in Mauritius in July 2014 was conducted to obtain updated information on the extent of antimicrobial resistance in the country

Methods & Materials: Results of all specimens of urine, pus swab, blood culture, tracheal secretion and intravascular catheter originating from hospital wards and processed at the Central Health Laboratory and at Jeetoo Hospital Laboratory in July 2014 were reviewed and analysed. Duplicate isolates from the same patient were excluded. Organisms considered likely to be normal flora or contaminants were not considered.

Results: Of 686 gram-negative bacteria recorded, the most common were *E.coli* (183), *Klebsiella* spp. (118), *Pseudomonas aeruginosa* (93), *Acinetobacter* spp. (78) and *Proteus* spp. (61). Most isolates were obtained from pus swabs (47%) and urine (25%) but tracheal secretion was the source of 32% of *Acinetobacter* spp. Percentage susceptibility to cefotaxime, ciprofloxacin, gentamicin, amikacin, meropenem and colistin was 54%, 42%, 73%, 93%, 97% and 100% respectively in *E.coli*, with corresponding figures of 42%, 47%, 57%, 81%, 91% and 100% respectively in *Klebsiella* spp., 6%, 18%, 21%,42%, 26% and 100% respectively in *Acinetobacter* spp., and 64%, 72%, 64%, 89%, 100% and 0% respectively in *Proteus* spp. Less than three-quarters of *P. aeruginosa* isolates were susceptible to gentamicin (58%), ciprofloxacin (53%), ceftazidime (70%), amikacin (71%), imipenem (73%) and meropenem (73%) but 89% were susceptible to piperacillin-tazobactam combination and 100% to colistin. Of 308 significant Gram-positive isolates recorded, *Staphylococcus aureus* (140) and *Enterococcus* spp. (96) were most commonly encountered. Only 61% of *S. aureus* isolates were susceptible to methicillin, but 69% and 100% were susceptible to erythromycin and vancomycin respectively. *S.aureus* was isolated from blood cultures of 27 patients, of which 5 (19%) were methicillin-resistant (MRSA). Of 96 enterococci recorded, 92% were susceptible to ampicillin and none was vancomycin-resistant.

Conclusion: Resistance to broad-spectrum antibiotics is common among Gram-negative bacteria and *S.aureus* isolated from hospitalised patients in Mauritius. Therapeutic options to treat many infections in hospitalized patients are now limited. There is a need for effective infection control and antibiotic stewardship programs to slow the emergence and spread of microorganisms with acquired resistance mechanisms.

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